Applications of Genetic Algorithms on theoretical fully-autonomous road systems

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Todo list

check onenote notebook for general ideas about discussion topics etc. . 2
Lay out different tasks & steps of the project, identify subgoals 6
Move formal goal definitions to Evaluation? 6
This is wrong, correct this or remove it outright 8
Decide whether to keep this section 9
Expand definitions of operators used in implementation section 10
extend list to include all functions used 12
Should I change this superscript notation? subscript is being used to denote which control points are being considered. 16
make reference to this method being altered for use in my solution(in approach section?) 18
Talk about Kala's road space coordinate system & use of Bézier curves, move to Bézier subsection? 19
Pare this down? 19
is this even correct to say? 20
Complete this section 20
Replace with detailed description of implementation of operators, decisions e.g. allowed range for mutation of control points. 21
Have I actually explicitly stated the construction of my fitness function & referenced Kala for inspiration? 22
Technically this infeasible distance calculation has very slightly changed in implementation, is it worth redoing or just leave as is? 24
formatting 24
Talk about implmentation of Uniform mutation operator 27
refer to lit rev sections discussing approaches by Kala[1] and Cai & Peng [2] 28
verify this 29
cite this or remove it 30
phrasing? 31
Merge these first 2? 31
remove this sentence? 32
Title? 32
Should I define it as $\mathcal{R} = (I, R)$? 32
wordy? 32
do I need to make it more obvious that these algorithms are my own work? Are they clear enough? 35
title? 37
phrasing about s/e position calculation on alg 3 37
necessary? 37

decide whether to remove this, I am thinking yes but last para is interesting, maybe move to evaluation 38
Is this a clear way of formatting? I would reference the ID when talking about a plot. I would still include an image as a figure 39
Check units for planning time + add link to hosted dynamic version . 39
Check units for planning time + add link to hosted dynamic version . 39
Implement another crossover operator to talk about ? 42
Is this all too boring? 43
expand on this section, talk about issues of finding intersection, possible GPU applications 43
correct word? 43
does this need to be an enumerated list? 44
make mention of possible GPU implementations such at in [3], modern enterprise GPUs have around 4000-10000 cores, approximately the max number of curve splits and comparisons in a binary check of depth 6. Being able to do this in a single cycle would result in a huge speedup, paper uses Titan X 44
check onenote notebook for general ideas about discussion topics etc.

Abstract

Contents

1 Introduction **6**
- 1.1 Goals . . . 6
  - 1.1.1 Requirements . . . 7

2 Background **9**
- 2.1 Genetic Algorithms . . . 9
  - 2.1.1 History . . . 9
  - 2.1.2 Definition . . . 9
  - 2.1.3 Genetic Operators . . . 10
- 2.2 Bézier Curves . . . 14
  - 2.2.1 Formal Definition . . . 15
  - 2.2.2 Length of a Bézier curve . . . 16
  - 2.2.3 Subdivision of n-degree Bézier curves . . . 16
- 2.3 Fully Autonomous Road Networks . . . 17
- 2.4 Miscellaneous . . . 17
  - 2.4.1 Bounded Boxes . . . 17

3 Literature Review **18**
- 3.1 Genetic algorithms for route generation . . . 18
  - 3.1.1 Genetic algorithms for cooperative route generation . . . 18
- 3.2 Bézier curves for route generation . . . 19
- 3.3 Fully Autonomous Road Networks . . . 20

4 Approach **21**
- 4.1 Single Agent Approach . . . 21
  - 4.1.1 Individual Encoding . . . 21
  - 4.1.2 Population Generation . . . 21
  - 4.1.3 Fitness assessment . . . 22
  - 4.1.4 Genetic Operators . . . 26
- 4.2 Multi-agent Approach . . . 28
  - 4.2.1 Collision Detection . . . 29
- 4.3 Macro-Level Planning . . . 32
  - 4.3.1 Road Graph Construction . . . 32
  - 4.3.2 Macro-Route planning . . . 34
  - 4.3.3 Agent Grouping . . . 35
  - 4.3.4 Multi-agent route planning . . . 37
- 4.4 Language Choice . . . 38

5 Results **39**

6 Evaluation **41**
6.1 Genetic Algorithms 41
6.1.1 Genetic Operator Performance 41
6.2 Bézier Curves 43
6.2.1 Cooperative Planning 44

7 Conclusion **45**

Appendices **48**

1 Introduction

Lay out different tasks & steps of the project, identify subgoals

Move formal goal definitions to Evaluation?

1.1 Goals

The overarching goal of this project is to optimally route traffic in the setting of a fully-autonomous road system. This however, is an aspirational goal with many sub-requirements to be fulfilled before it can come to fruition.

Formally this top-level goal can be said to be to answer the question in Problem 1.

Top-level Goal

Input:

- A road system $\mathcal{R}$ represented as a graph $\mathcal{R} = (V, E)$

  Where each edge $e \in E$ is a section of road defined as the space between two vertices $v^1, v^2 \in V$ which is bounded by two functions $b_1(x)$ and $b_2(x)$ and augmented by a set of obstacles O representing infeasible sections of road space

- a set of agents, $A = \{a_1, \ldots, a_n\}$

- a list of vertex pairs representing start and goal points for each agent:

  $\mathcal{V} = \left\{(v_1^1, v_1^2), \ldots, (v_n^1, v_n^2)\right\}, v_{i\in[1\ldots n]}^{j\in[1,2]} \in V$

  where the route for agent a_i is from vertex v_i^1 to v_i^2

Question: What is the set of optimal routes $\sqsubseteq_{optimal}$, where the i^{th} element is defined as a set of linked Bézier curves connecting v_i^1 and v_i^2 through feasible space?

Problem 1

We can then split this into more manageable sub-goals. The sub-problem of generating a route through a section of road is defined in Problem 2. This

can be further decomposed into the selfish routing of a single agent through a section of road defined in Problem 3

Sub-Goal: Cooperative route planning

Input:

- A start point P_{start} and a goal point P_{goal}
- A section of road as defined in Problem 1
- A knowledge of all routes being planned to be executed concurrently.

Question: What is the optimal route, in the form of a Bézier curve, between these two points s.t. it does not collide with any other agents or pass through any infeasible regions in the road space?

Problem 2

Sub-Goal: Single agent route planning

Input:

- A start point P_{start} and a goal point P_{goal}
- A section of road as defined in Problem 1

Question: What is the optimal route, in the form of a Bézier curve, between these two points s.t. it does not pass through any infeasible regions in the road space?

Problem 3

1.1.1 Requirements

The goal of this project was not to produce a production-ready system, but instead, to investigate the plausibility of GAs on the real future possibility of completely autonomous road networks. As such I feel it useful to outline the theoretical requirements of a production grade system. To do this formally

Sub-Goal: Bézier curve generation

Input:

- A start point P_{start} and a goal point P_{goal}
- A section of road as defined in Problem 1

Question: What is the optimal route, in the form of a Bézier curve, between these two points s.t. it does not pass through any infeasible space?

Problem 4

I will employ Propositional and Temporal logic.

1. The system should never return a set of routes such that, for any time $t \in T, \forall i \in n, \forall j \in n, j \neq n, I_i(t) = I_j(t)$. I.e. for any time, no routes should inhabit the same point, meaning there are no collisions in the planned routes.

This is wrong, correct this or remove it outright

2 Background

2.1 Genetic Algorithms

2.1.1 History

Decide whether to keep this section

Genetic algorithms (GAs) are a type of meta-heuristic optimisation technique that employ the same rationale as classical evolution seen in nature.

Genetic Algorithms can trace their origins back to the late 1960s when they were first proposed by John Holland, though he then referred to them as *Genetic Plans*[1]. Holland went on to write the first book on the subject titled *Adaptation in Natural and Artificial Systems*[4] in 1975. The field did not find much reception with Holland stating in the preface to the 1992 rerun:

> *"When this book was originally published I was very optimistic, envisioning extensive reviews and a kind of 'best seller' in the realm of monographs. Alas! That did not happen."*

However, in the early nineties, Genetic algorithms surged in popularity along with the area of Artificially Intelligent planning as a whole, leading to Holland republishing his book and solidifying his position as the field's founder.

2.1.2 Definition

In a general sense, optimisation techniques work to find the set of parameters $\mathcal{P}$ that minimise an objective function $\mathcal{F}$. Genetic algorithms approach this by representing these sets as individuals in a population, P. Over the course of multiple generations, the best solutions are determined and promoted until termination criteria are met or the maximum number of generations is reached.

As our candidates are essentially a collection of parameters to the function we are trying to optimise, we can extend our metaphor further by mapping each element of a individual to a *gene* in a individual's genome.

The representation we use in a GA is problem specific. Often we have to provide functions to facilitate the mapping between the problem specific set of possible solutions and the encoded genotype space in which we optimise. The most basic representation being a string of binary numbers.

An individual's characteristics and genetic information is normally encapsulated within the Phenotype. Here not only the genetic information of

[1] This distinction was made to emphasise the *"centrality of computation in defining and implementing the plans"* [4]

the Genotype but also additional information, such as fitness, is stored in order to prevent it from being re-calculated as often.

In general, an individual's phenotype is the real-world representation of the candidate solution. The genotype is the low-level representation on which the genetic operators can operate. I will generally refer to both as an individual throughout this paper as the distinction is only necessary at the implementation level.

Genetic algorithms are both *probabilistically optimal* and *probabilistically complete*[1] meaning that: given infinite time, not only will the algorithm find *a* solution, (if one exists), it will find **the** optimal solution from the set of all possible solutions, $\mathcal{P}^*$.

Algorithm 1: Modern Generic Genetic Algorithm

Result: Best Solution, $p_{\texttt{best}}$
Generate initial population, P_0 of size n;
Evaluate fitness of each individual in P_0, $\{F(p_{0,1}, \ldots, p_{0,n})\}$;
while *termination criteria are not met* **do**
  Selection: Select individuals from P_t based on their fitness;
  Variation: Apply variation operators to parents from P_t to produce offspring;
  Evaluation: Evaluate the fitness of the newly bred individuals;
  Reproduction: Generate a new population P_{t+1} using individuals from P_t as well as the newly bred candidates.;
  t++
end
return $p_{\texttt{best}}$

As you can see from Figure 2.1 and Algorithm 1 the overall shape of GAs has not changed substantially over the course of the past 50 years. Being comprised of a series of operations that a starting population is piped through until criteria are met.

2.1.3 Genetic Operators

In the following section I will outline the various genetic operations that take place in a GA, they can be seen in Algorithm 1. Any operators used and analysed in Chapter 4 will have more detailed explanations of their process.

Expand definitions of operators used in implementation section

Selection

The selection procedure is the process by which the next generation of individuals is created from the current population. Individuals are selected relative to their fitness as determined by the Objective (fitness) function $\mathcal{F}$.

Some methods select only the best solutions by fitness. Others employ a more stochastic approach, such as roulette wheel selection, to increase diversity and reduce complexity.

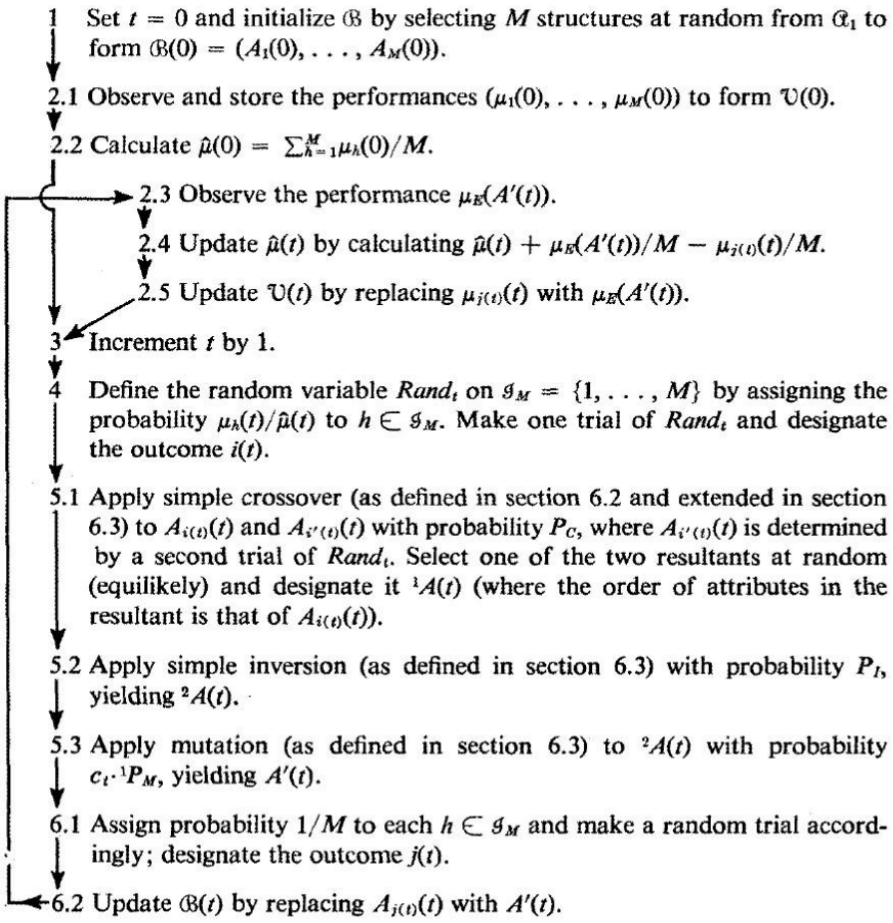


Figure 2.1: GA outlined in Holland's Original Book[4]

Fitness Proportional Selection Fitness proportional or Roulette wheel selection is a popular selection operator. It uses fitness to assign selection probability to each individual in a population.

The probability of selection for an individual i with fitness $\mathcal{F}(i)$ can be expressed mathematically as:

$$p_i = \frac{\mathcal{F}(i)}{\sum_{j=1}^{N} \mathcal{F}(j)} \tag{2.1}$$

Where N is the size of the population P

This is a simple approach but performs well and has very little performance overhead.

Ranked Selection Ranked selection is an alternative selection method, it works on the assumption that the individuals in your population are closely grouped in fitness. The main difference of this method when compared to fitness proportional selection is that it ranks individuals based on relative fitness rather than absolute fitness.

The procedure can be written mathematically as:

Given a population P of size n ordered by fitness. We select the top γ-ranked individual, x_γ with a probability $p(\gamma)$. Where γ is the rank and $p(\gamma)$ is the ranking function.

The ranking function can take different forms including both linear and exponential ranking.

extend list to include all functions used

Linear ranking is defined as:

$$p(\gamma) = \frac{\alpha + (\beta - \alpha) \cdot \frac{\gamma}{n-1}}{n} \tag{2.2}$$

Where:

- $\sum_{\gamma=0}^{n} p(\gamma) = 1$
- $\alpha + \beta = 2$
- $1 \leq \beta \leq 2$

Variation

Variation in a GA is the process of altering the genome individuals to further explore the search space via stochastic local search. We perform this using two distinct sub-operations: Mutation and Crossover. Here we can view crossover as the *breeding* process and mutation as resembling the natural tendency for DNA to mutate over the course of generations.

Mutation In mutation we alter each gene with a set probability p_m known as the *mutation rate*. A standard value for a mutation rate is $\frac{1}{L}$ but it can fall anywhere in the range $p_m \in [\frac{1}{L}, \frac{1}{2}]$ where L is the length of the genome.

A low value for p_m a new individual which can be shown to be *close* to it's parents in the search space relative to their *Hamming distance*[2] if using a Binary coded GA. In real-coded GAs they can be shown to be close by the Euclidean distance between them.

In binary coded GAs we alter a given gene by *flipping* it's value. In real-coded GAs mutation operators include:

- Uniform Mutation
- Non-Uniform Mutation
- Gaussian Mutation

Uniform Mutation In uniform mutation, we select a parent p at random and replace a randomly selected gene $c_i \in p$ with a uniformly random number $c_i' \in [u_i, v_i]$ where u_i and v_i are set bounds.

Gaussian Mutation In Gaussian mutation, we select a parent p at random and randomly select a gene $c_i \in p$. We replace c_i with a new value c_i' which is calculated as follows:

$$c_i' = \min(\max(\mathcal{N}(c_i, \sigma_i), u_i), v_i) \tag{2.3}$$

Where $\mathcal{N}(c_i, \sigma_i)$ is a Gaussian distribution with a standard deviation σ_i and a mean of c_i. σ_i may depend on the length of the interval bound, $l_i = v_i - u_i$, typically (and in my implementation) $\sigma_i = \frac{1}{10} l_i$

Crossover

Crossover is a binary operation, taking two randomly selected *parents* from the population P_t with a probability $p_c \in [0, 1]$

There are two major forms of crossover for binary coded GAs: $n > 1$ point crossover and Uniform crossover.

For real-coded GAs you instead have a selection of Crossover operators including:

- Flat crossover
- Simple crossover
- Whole arithmetic crossover

[2]Hamming Distance: A metric for comparing two binary data strings. The Hamming distance between two strings is the number of bit position in which they differ.

- Local arithmetic crossover
- Single arithmetic crossover
- BLX-α crossover

Simple (one point) Crossover For simple crossover, randomly select a crossover point, $i \in \{1, \ldots, n\}$. All values before this point are swapped between the two parents. For 2 parents, $p_1 = \left\{x_1^{[1]}, \ldots, x_n^{[1]}\right\}$ and $p_2 = \left\{x_1^{[2]}, \ldots, x_n^{[2]}\right\}$ this can be represented as:

$$p_1' = \left\{x_1^{[1]}, x_2^{[1]}, \ldots, x_i^{[1]}, x_{i+1}^{[2]}, \ldots, x_n^{[2]}\right\} \tag{2.4}$$

$$p_2' = \left\{x_1^{[2]}, x_2^{[2]}, \ldots, x_i^{[2]}, x_{i+1}^{[1]}, \ldots, x_n^{[1]}\right\} \tag{2.5}$$

Evaluation

After developing potential new individuals, the fitness of these new individuals is calculated using the objective function, $\mathcal{F}$

Reproduction

Here the next generation of individuals is constructed. There are multiple potential methods employed here with the simplest being to just replace the lest fit individuals with additional copies of the fitter individuals, be they pre-existing or newly generated.

In this stage various heuristics or alternative strategies can be implemented to speed up or slow down the convergence rate. Whilst their fitness may be low, having a diverse population allows for more of the search space to be explored. If the algorithm converges too quickly it may get *stuck* in local minima.

2.2 Bézier Curves

In my implementation, I utilise Bézier curves to encode complex route arcs between a series of points. Here I will briefly outline their construction and mathematical basis.

Bézier curves were popularised by and named after French auto-body[3] designer Pierre Bézier in the 1960s and are commonly found in computer graphics today. They are parametric curves made up of a series of *control points* which contort the shape of a line to produce a curve of nearly any

[3] so I feel it is quite fitting that they find use in 21^{st} century automotive problems

shape. Although their mathematical basis was established in 1912 by Sergei Bernstein in the form of Bernstein polynomials[5].

A Bézier curve is said to have a degree of $n-1$ where n is the number of control points including the start and end point of the curve.

2.2.1 Formal Definition

Bézier curves can be simply explicitly defined for degrees of 1 through 4, however, the general case of n points is more useful to us. In their general form they can be defined recursively or explicitly. I implement the recursive version as it is much more readable for a programming language that supports recursion.

They are defined recursively as follows:

$$\mathbf{B}_{P_0}(t) = P_0 \tag{2.6}$$

$$\mathbf{B}_{P_0,P_1,\ldots,P_n}(t) = (1-t)\mathbf{B}_{P_0,P_1,\ldots,P_{n-1}}(t) + t\mathbf{B}_{P_1,P_2,\ldots,P_n}(t) \tag{2.7}$$

Where the initial curve $B = B_{P_0,P_1,\ldots,P_n}$ and the parameter t is a real number in the range of $[0,1]$. Therefore, the smoothness of the curve is determined by the granularity of the parameter when realising the curve.

An example of how the parameter t corresponds to points on the curve can be seen in Figure 2.2, the red numbers indicate the value for t that corresponds to the green points on the curve and the purple points correspond to the control points. I.e. $B(0.37)$ produces the coordinates for the first labelled point seen, where the curve shown is B.

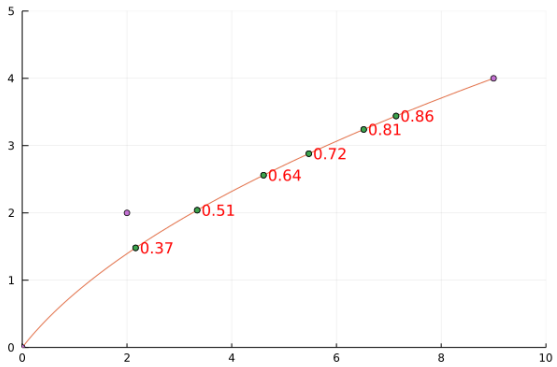


Figure 2.2: Example of a Bézier curve with a random sample of points

2.2.2 Length of a Bézier curve

The length of a Bézier curve is a non-trivial calculation and is best approximated as:

$$L = \frac{(2L_c + (n-1)L_p)}{n+1} \tag{2.8}$$

Where L_c is chord length and L_p is polygon length. This was proven by Jens Gravesen[6] in 1997.

Chord length is given by:

$$L_c = \sqrt{(P_{0_x} - P_{n_x})^2 + \left(P_{0_y} - P_{n_y}\right)^2} \tag{2.9}$$

and polygon length by:

$$L_p = \sum_{i=0}^{n-1} \sqrt{(P_{i_x} - P_{i+1_x})^2 + \left(P_{i_y} - P_{i_y}\right)^2} \tag{2.10}$$

Or, alternatively:

$$L_p = \sum_{i=0}^{n-1} L_c(B_{P_i,P_{i+1}}) \tag{2.11}$$

2.2.3 Subdivision of n-degree Bézier curves

Subdivision of Bézier curves is a key stage in the process of finding any intersections between two Bézier curves. The process of subdivision is performed using De Casteljau's algorithm. This algorithm was developed by Paul de Casteljau while working at Citroen in 1959 to work with the family of curves that would later be formalised into Bézier curves by Pierre Bézier[4].

It is a simple procedure, given a Bézier curve B, it can be split at any arbitrary point $t \in [0, 1]$ into two curves with control points of the form:

$$\beta_1 = B_{P_0}(t), B_{P_0,P_1}(t), \ldots, B_{P_0,\ldots,P_n}(t) \tag{2.12}$$

$$\beta_2 = B_{P_n}(1-t), B_{P_n,P_{n-1}}(1-t), \ldots, B_{P_n,\ldots,P_0}(1-t) \tag{2.13}$$

Should I change this superscript notation? subscript is being used to denote which control points are being considered.

[4]Bézier curves have also been called de Casteljau curves as much of his work preceded that of Pierre Bézier's

2.3 Fully Autonomous Road Networks

Fully autonomous road networks are by no means a novel concept. They have appeared in fiction since the mid 20th century and have been a real possibility for the past decade. In a fully autonomous road networks *(FARN)*s, all vehicles are self-operating with their routing either being determined on a vehicle-by-vehicle *selfish* basis or by a larger system managing routes for all nearby agents.

In the latter system protocols that promote the net increase in efficiency can be implemented. However, this sort of system will require a form of government mandate as a universal routing protocol would need to be established and implemented by all auto manufacturers; this is no small undertaking.

2.4 Miscellaneous

2.4.1 Bounded Boxes

A bounded box of a curve is defined as the box constructed from the points $(x_{min}, y_{min}), (x_{min}, y_{max}), (x_{max}, y_{min}), (x_{max}, y_{max})$ Where $x_{min,max}$ and $y_{min,max}$ are the minimum and maximum x and y values from all control points respectively. An example can be seen in Figure 2.3

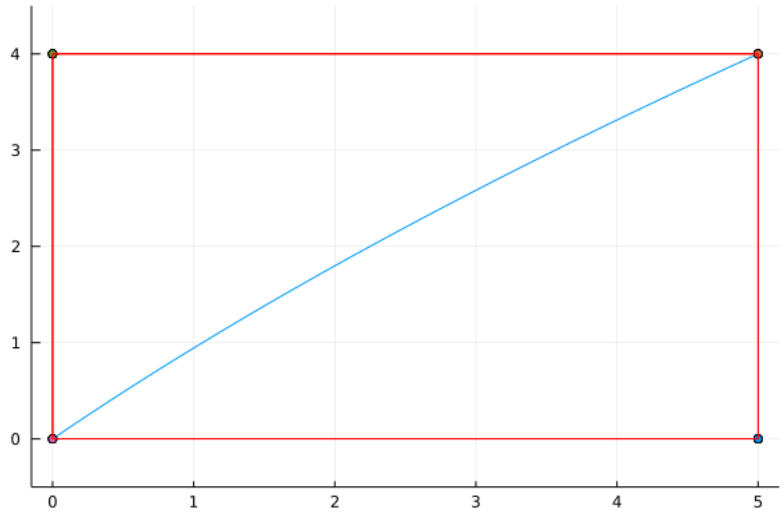


Figure 2.3: A bounding box for a Bézier curve of degree 2

3 Literature Review

3.1 Genetic algorithms for route generation

Classical Genetic algorithms have seen research and applications in a number of fields over the past 40 years ranging from Heart disease diagnosis[7] to predicting the strength of concrete under various conditions[8].

There is a substantial and growing body of research specifically looking at the applications of GAs in route planning for autonomous agents, however, many are focusing on either abstract robotic agent planning in discrete search spaces or failing to take into account the wider environment of multiple agents.

3.1.1 Genetic algorithms for cooperative route generation

Cai & Peng - Cooperative Coevolutionary Adaptive Genetic Algorithm in Path Planning of Cooperative Multi-Mobile Robot Systems[2] In this 2001 paper, Cai & Peng give an example of a Cooperative Coevolutionary Adaptive Genetic Algorithm (CCAGA) for planning routes for multiple autonomous agents.

Their approach features a discrete grid-based search space featuring rectangular obstacles which the routes must avoid. Their chromosomes are encoded using real-values representing the x and y coordinates of the search grid.

Their fitness function has two stages, in the first generation the fitness of a candidate solution is purely determined by the global *optimality* of the route. In all subsequent generations the fitness also takes into account the best routes from each of the other sub-populations.

They conclude that their approach yields good robustness and convergence as well as being suitable for parallel execution, allowing for systems employing this GA approach to run very efficiently.

make reference to this method being altered for use in my solution(in approach section?)

Raul Kala - Optimization Based Planning 2016[9] In his book, Kala proposes a GA as an embedded component of a larger planning system which also relies on Djiksra's algorithm for macro-level route planning along with the classical autonomous vehicle real-time collision avoidance toolbox (radarr, sonarr, etc.). In order to achieve a system capable of planning for multiple agents concurrently, Kala proposed the use of these real-time collision avoidance tools along with embedding *traffic rules* as heuristics into the Djiksta-based component. These traffic rules included "driving on the left" and "overtaking on the right" etc. This proposed system, while similar

to mine, differs in scope. I propose a system for planning routes for a set of autonomous agents within a fully-autonomous road system, meaning agents will not (in theory) interact or encounter any other vehicles which are not a part of the planning network.

Talk about Kala's road space coordinate system & use of Bézier curves, move to Bézier subsection?

Cruz-Piris et al. - Automated Optimsization of Intersections Using a Genetic Algorithm[10] A paper published by Cruz-Piris et al. investigates the applications of (binary coded) Genetic Algorithms on routing traffic through busy intersections. Their proposed system is shown to have improvements in traffic throughput of anywhere from 9% to 36%.

Their approach involved several assumptions, many of which my research shares. Namely, they assumed vehicles do not stop at any point and that their speed remains constant at all points in time.

Their approach to modelling the solution space takes advantage of the fairly uniform and regular structure of large intersections, and although they work on modelling irregularly shaped intersections, this TCA model begins to fall apart when the size of each cell cannot contain a vehicle and requisite surrounding space or if input/output lanes do not lie in a regular grid pattern. Facilitating irregularly shaped intersections seems to be a manual process, not a particularly viable method when you consider the number of unique intersections across the world or even just the Continental United States!

Pare this down?

This approach seems to work relatively well for throughput optimisation problems such as junctions but does not scale well for less structured scenarios where all origins and goals cannot be known beforehand and are not necessarily the same for all subsequent runs.

Roberge et al. - Fast Genetic Algorithm Path Planner for Fixed-Wing Military UAV Using GPU[3] In this 2018 paper an interesting proposition was made, greatly increasing efficiency and viability of real-time planning via GAs through massively parallelising its core processes to run on GPUs. Their implementation shows a 290x times speedup compared with conventional sequential CPU execution. GAs lend themselves quite nicely to parallel execution as we are applying the same operators to multiple individuals of the same shape.

3.2 Bézier curves for route generation

Chen et al. - Quartic Bézier Curve based Trajectory Generation for Autonomous Vehicles with Curvature and Velocity Constraints In this 2014 paper, Chen et. al research the efficacy of quartic (4-degree) Bézier curves for planning continuous routes between points for autonomous vehicles. In order to find an optimal solution they employ sequential quadratic programming.

In their approach Chen et al. also take into account the orientation, change in orientation and velocity of the routes generated in order to assure all generated routes are *safe* for occupied vehicles to follow.

This approach appears to be extremely computationally efficient on the toy examples provided in the paper, on relatively low performance hardware 560 iterations can be computed in around 500ms!

There is no mention, however, to a cooperative element. Explicitly solving quadratic programming tasks is known to be **NP**-complete as shown by Vavasis in 1990[11] and adding onto that the requirement that all solutions interact nicely will only increase the real-world runtime of any solution. A real-world scenario with hundreds of vehicles may suffer from an incredibly high runtime, hardware requirement or both.

is this even correct to say?

3.3 Fully Autonomous Road Networks

Complete this section

Fully Autonomous Road Networks (*FARN*s) have the possibility of improving travel in a number of different areas.

They have the potential of greatly reducing travel times by efficiently routing all vehicles with the goal of reducing the net travel time. Such a system would also be able to respond much faster than human drivers, allowing for large increases in permissible vehicle velocities thus, further increasing efficiency.

By extension of their higher efficiency, *FARN*s will also have a marked effect on vehicular energy consumption. The potential effects are summarised nicely by Vahidi and Sciarretta[12] where they show the use of vehicle automation could cause anywhere from a halving of "energy use and greenhouse gas emission" in an "optimistic scenario" to doubling them depending on the effects that present themselves such as reduced public transport usage. The increase in highway speed whilst increasing travel efficiency is predicted by Brown et al.[13] and Wadud et al.[14] as increasing energy use by anywhere from 5% to 30%.

4 Approach

4.1 Single Agent Approach

The goal of this section was to design a system that fulfilled the requirements outlined in Problem 3

The general shape of a GA as seen in Algorithm 1 is the same for almost all problems. But each individual operator implementation is domain specific.

4.1.1 Individual Encoding

As such, I first had to implement a method to generate an initial population. In order to do this, I had to define my programmatic representations of the phenotypes and genotypes of my individuals. I decided to base my pheno and genotypic structure on the that described by Kala[1].

In this approach, the phenotype is abstractly represented as a Bézier curve (Section 2.2). This is more concretely translated into a genotype encoded as a real-valued string, interleaving the x and y coordinates of each control point. Taking the form:

P_{0_x}	P_{0_y}	P_{1_x}	P_{1_y}	$\cdots$	P_{n_x}	P_{n_y}

Figure 4.1: Individual genotype as real-valued string

In the above form the descriptions of genetic operators found in Section 2.1.3 should be sufficiently detailed to re-implement.

Replace with detailed description of implementation of operators, decisions e.g. allowed range for mutation of control points.

Initially my Phenotype contained no additional information. However, I still created the distinction to allow for additional properties to be encapsulated during development.

4.1.2 Population Generation

Population generation theoretically can be very simple and generate very little diversity, relying on the other operators to explore the search space. However, the more diverse a set of initial routes one can generate, the quicker the system will converge to an optimal solution.

As such we want to ensure that both the number of control points as well as their position are properly varied.

The first and last control points **must** be the starting and goal position for the agent. In a Bézier curve these are the only two points that the curve definitely passes through. We must also ensure that the x coordinates of the control points are in order, so as to avoid routes which *double back* on themselves. This can also occur as the result of other operators such as crossover and mutation, we can fix this using a simple repair operator which re-orders points based on their x positions.

Once the initial population is generated, the main algorithmic loop can begin, this is the repeated application of the selection, crossover, mutation and evaluation operators (See Section 2.1.3) until set termination criteria are met or the maximum number of generations is completed, seen in Algorithm 1.

4.1.3 Fitness assessment

Have I actually explicitly stated the construction of my fitness function & referenced Kala for inspiration?

The foundation of my Fitness function is the length of each route, i.e. the length of a given n degree Bézier curve. This calculation can be accurately approximated using Equation 2.9 as the true calculation is expensive and does not generalise nicely to n degrees[6].

Minimising the length of a route is a good way of ensuring generated routes are direct, however, other values and heuristics are required to maintain other requirements such as to make sure changes in direction are not too severe or that a route does not pass through infeasible space (avoiding obstacles etc.).

Road Section Definition

I initially experimented with an alternative coordinate space which enabled me to completely enclose the search space within the area of the road, eliminating the possibility of generating routes that left the *road*. This was inspired by the "Road coordinate axis system" described by Kala in [9]. However I abandoned this concept as it did not appear to increase performance and introduced overhead when visualising or generating the routes.

Instead I defined each section of road using the following Structure:

```
struct Road
    boundary_1::Function
    boundary_2::Function
    obstacles::Array{Obstacle}
    length::Real
end
```

This approach allows me to define the upper and lower boundary of a road as any function, straight roads can be defined as a pair of straight lines a certain width apart, and arbitrarily complex roads can be represented using arbitrarily complicated functions.

For example the road seen in Figure 4.2 had boundary functions:

$$b_1(x) = 0$$
$$b_2(x) = 5$$

And the curved road section seen in Figure 4.3 functions:

$$b_1(x) = 2\cosh(0.1x) - 2$$
$$b_2(x) = 2\cosh(0.12x) + 8$$

Where in both cases the length of the road (and therefore upper bound of x) was 25, the lower bound of x was 0.

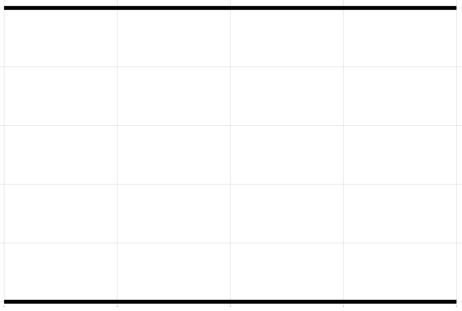


Figure 4.2: A straight road

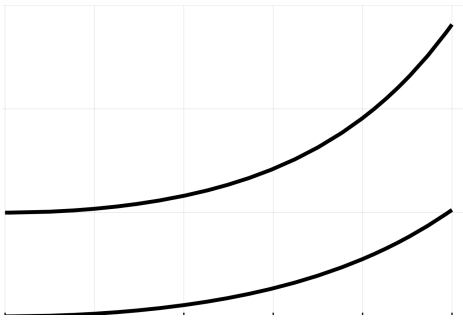


Figure 4.3: A curved road

Road Obstacles I have implemented two basic `Obstacle` types (`Rectangle` and `Circle`) allowing me to create regions of infeasible space within the valid road-space.

Infeasible space is then calculated by taking a sample of 500 points along a given curve B and checking which (if any) lie within any of the obstacles.

A Bézier curve is then constructed using two applications of De Casteljau's algorithm (See Section 2.2.3) using values for t derived from the sub-sample points. An illustration of this process can be seen in Figure 4.4. The length of this curve is weighted and added to the overall fitness of the candidate solution. The stages progress as Follows:

1. Curve and obstacle drawn
2. Uniform sample of points chosen along curve
3. Curve segment from origin to first infeasible point isolated
4. Curve segment from last infeasible point to end position isolated
5. Infeasible distance calculated as difference in length between original curve and two isolated segments

A similar process is performed to determine how much of a curve passes too closely to an infeasible region, this is penalised with a separate, lower, weighting.

Technically this infeasible distance calculation has very slightly changed in implementation, is it worth redoing or just leave as is?

Now with the ability to calculate the length of a route as well as the distance it travels through/ too close to infeasible space, I can define my Fitness function:

$$\mathcal{F}(i) = L_i + \alpha \cdot \texttt{infeasible distance}(i) + \beta \cdot \texttt{high-proximity distance}(i) \quad (4.1)$$

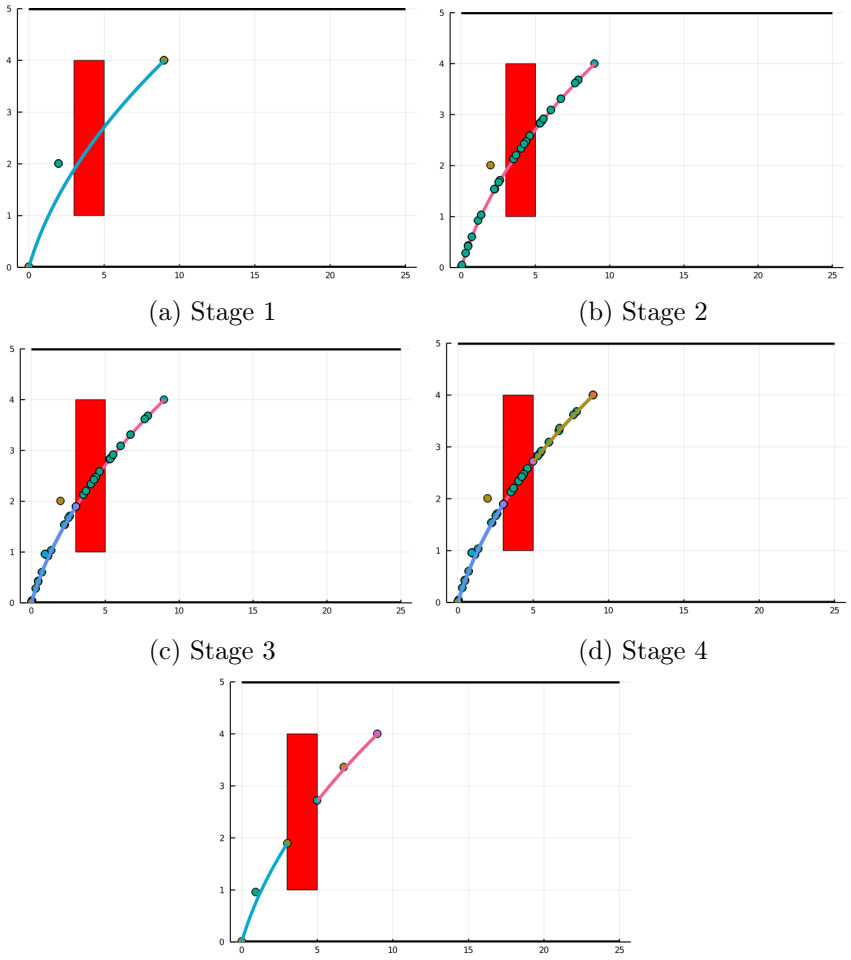
formatting

Where:

- L_i is the length of candidate i's route
- α and β are weighting parameters s.t.

  $\alpha > \beta > 1$

  therefore penalising infeasible distance harder than distance which is *too close* to infeasible space, guiding the GA to prioritise avoiding infeasible space.



(a) Stage 1

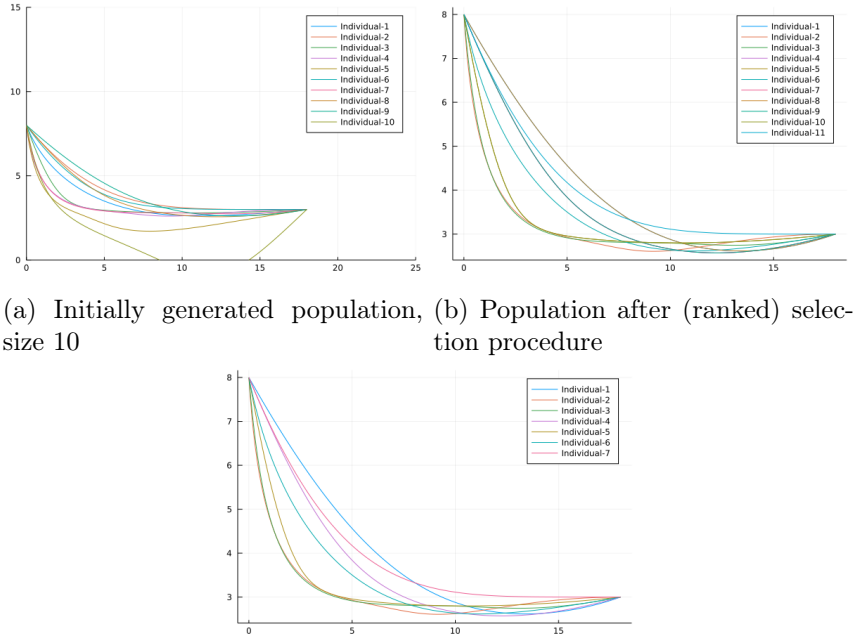
(b) Stage 2

(c) Stage 3

(d) Stage 4

(e) Stage 5

Figure 4.4: Illustration of finding infeasible section of curve



(a) Initially generated population, size 10

(b) Population after (ranked) selection procedure

(c) Population after (ranked) selection procedure, duplicates removed

Figure 4.5: Example of ranked selection

This function is inspired by Kala[9] and proves to be a good basis for a naive single agent planner, futher augmentation is required to support multiple agents or variable velocity profiles.

4.1.4 Genetic Operators

The abstract goal of each genetic operator has already been discussed in Section 2.1.3. Here I will discuss their concrete implementation with respect to my task.

Selection

My selection procedure follows very closely to the method outlined in Section 2.1.3, relying on the fitness function to duplicate fit individuals, replacing the less fit ones with a certain chance or reasoning.

An example of ranked selection on a sample population can be seen in Figure 4.5

Mutation

The variants of the mutation operator that I have implemented are Uniform and Gaussian. Both attempt to achieve the same effect via different methods.

Abstractly, my mutation operators select a control point with a random probability and mutate within fixed bounds. These bounds are tied to the size and shape of the road.

In my Gaussian mutation operator, the range of x values for the mutation of a randomly selected point $p \in B = \{p_1, \ldots, p_n\}, n \in \mathbb{Z}^{\geq 2}$ are:

$$\mathcal{X} = [p_{1_x}, p_{n_x}], p_1, p_n \in B \tag{4.2}$$

I.e. a mutated control point cannot lie before or after the start or end points respectively. The range of y values a mutated point can take is within:

$$\mathcal{Y} = \left[-1.3 \cdot \frac{b_1(\mathcal{X}_1) + b_2(\mathcal{X}_2)}{2}, 1.3 \cdot \frac{b_2(\mathcal{X}_1) + b_2(\mathcal{X}_2)}{2}\right] \tag{4.3}$$

Meaning -1.3 times the average y coordinate of the bottom road boundary to 1.3 times the average of the top road boundary across the range of permitted x values. ± 1.3 was used after experimenting with values ranging from ± 2 to ± 0.5, 1.3 offers the procedure the chance to significantly affect the course of a route whilst minimising the chance that the mutated route will be infeasible.

A pair standard deviations as previously outlined in the Background section are defined as:

$$\sigma_x = \frac{\mathcal{X}_1 - \mathcal{X}_2}{10} \tag{4.4}$$

$$\sigma_y = \frac{\mathcal{Y}_1 - \mathcal{Y}_2}{10} \tag{4.5}$$

A new point, p', is then constructed as follows:

$$p'_x = \min(\max(\mathcal{N}(p_x, \sigma_x), \mathcal{X}_1), \mathcal{X}_2) \tag{4.6}$$

$$p'_y = \min(\max(\mathcal{N}(p_y, \sigma_y), \mathcal{Y}_1), \mathcal{Y}_2) \tag{4.7}$$

Point $p \in B$ is then replaced with our new point p'.

The result of the operation being applied to a example curve can be seen in Figure 4.6

Talk about implmentation of Uniform mutation operator

Crossover

Simple crossover is implemented as it is described in Section 2.1.3, two parents are randomly selected and exchange genotypic information about a random point. I have been careful not to choose a crossover point which splits a control point. The result of this operation is appended to the current population, only the top n individuals are carried forward to the next generation. Once used to create offspring, an individual cannot again participate

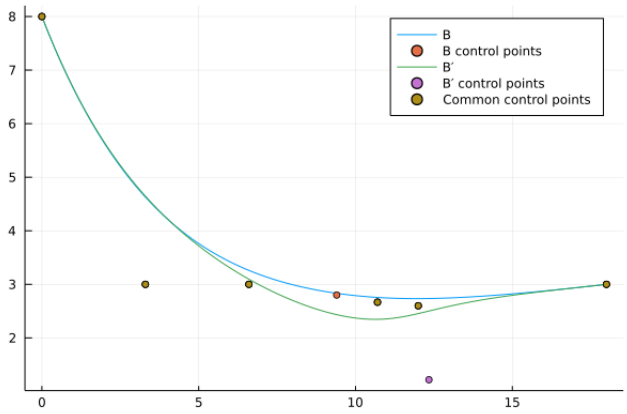
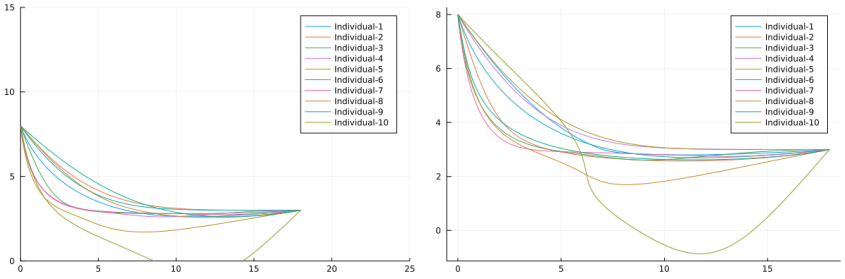


Figure 4.6: Example of Gaussian mutation on a Bézier curve



(a) Initially generated population, size 10

(b) Population after crossover operation is applied

Figure 4.7: Example of simple crossover

in crossover, however, duplicate individuals created via the selection process may effectively reproduce multiple times.

The result of a single (simple) crossover operation can be seen in Figure 4.7

4.2 Multi-agent Approach

So far we have only concerned ourselves with planning a route through a road-space for a single agent. However, in the real world, roads are seldom occupied by a single vehicle and as such we must consider how to efficiently plan a set of routes for a set of agents between between a set of coordinate pairs, such that, our agents do not collide at any point in time.

There are different approaches we can take to this problem.

refer to lit rev sections discussing approaches by Kala[1] and Cai & Peng [2]

My initial approach to a collaborative planning system was somewhat inefficient. The system operated by planning routes for each agent sequentially, using a growing *context* to keep track of the routes that had already been finalised. The first agent to be planned was not concerned with avoiding collisions, as, as far as it was concerned, there were no other agents in the system. Each subsequent agent checked if any of its candidate solutions intersected with and of the routes planned before, a very high penalty was applied to any routes with collisions.

This system was very inefficient with the final routes requiring a large number of checks to be carried out by my `bezInt` function, which itself suffered from

verify this

exponential time (and space) complexity.

This system was improved upon by splitting the process over multiple threads, each agent being given a separate thread, communicating their most up-to-date plans via a shared array, S. Agent i will store its current fittest route in $S[i]$, the calculation for fitness of any candidate checks for collisions with each route in S. This system may conduct more checks but it removes the problem of prioritising the first route to the planned and reduces the overall runtime of the system approximately proportionally to the number of threads available, an abstract view of the topology can be seen in Figure 4.8 with each agent $a_k, k \in [1, n]$ being mapped to a separate threaded instance of my GA planner. Each instance has access to the shared array which stores the fittest route after generation $i \in [1, m]$ with m being the maximum number of generations for each agent.

Updates to the shared array happen as and when each thread reaches the end of a generation. This can mean that routes that terminate before others have to adapt less to other routes, but this trade-off cannot be avoided without instituting constant communication between threads, which in and of itself introduces overhead and slows down planning.

4.2.1 Collision Detection

Collision detection is one of the core obstacles to a viable cooperative route planner. You must be able to certify that your resulting set of routes do not collide at any point in time, else the entire system fails.

Simply detecting intersections is not enough as two routes can intersect but only collide if they pass through the same point at the same time. We therefore require some notion of time when realising our Bézier curve routes.

I made the assumption that each agent in my system travels at a uniform constant speed. To remove this assumption we would need to include a velocity-time profile in the genotype of each individual, this is an area for further research.

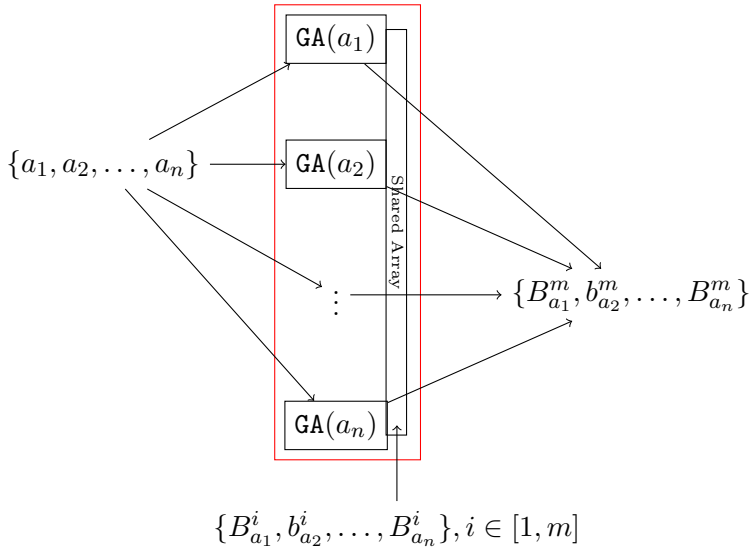


Figure 4.8: Parallel Cooperative Genetic Algorithm abstract topology

With this assumption, we can now say that two routes collide if they intersect and the distance from their respective origins and the point of intersection is the same (or below a threshold). We have now reduced this problem to finding a point of intersection between two Bézier curves, this is still a non-trivial task.

Bézier Curve intersection

The commonly employed technique for finding intersections between two n-degree Bézier curves is repeated recursive subdivision. Whilst it is possible to precisely calculate the point of intersection it is very difficult and computationally expensive and does not generalise well to n degrees. For example, to numerically find the intersection two curves of degree 3 we must solve a 9^{th} order equation, producing unstable results. This is described by Bézout's theorem which states that two planar algebraic curves of degrees d_1 and d_2 will have up to $d_1 d_2$ intersection points.

cite this or remove it

In their 2006 paper Yap[15] proposed an efficient method for finding the intersection of two Bézier curves through a 2 stage process surrounding repeated subdivision.

During development I attempted to use a Bézier curve library (`libbezier`)[16] written for python but featuring a core written in Fortran, providing a C ABI. Julia, featuring interoperability with C and Fortran, allowed me to make direct calls to the Fortran subroutines and C functions. Ultimately, however, I encountered too many issues stemming from this library's inability to be run in parallel along with seemingly random segfaults which I struggled to

diagnose through two levels of language abstraction (Fortran → C → Julia); this led me to write my own functions natively in Julia, although replicating the same accuracy as the nearly 4000 lines of Fortran proved challenging.

In order to speedup my Bézier intersection function I implemented a number of time saving measures:

1. If the convex hulls of two curves B_1 and B_2 intersect, i.e. some amount of the area of the convex hull of B_1 ($CH(B_1)$), lies inside the convex hull of B_2 ($CH(B_2)$) then there may be some intersection and as such, further checks are required. If however, this is not the case then (likely) the two curves do not intersect and the function can exit early.

   This is a simplified version of the logic presented by Yap in his *Micro Phase* of intersection detection. However, in order to cover all edge cases and make this a reliable rule to follow a lot more precomputation is required (See Elementary curves & curve coupling in [15]).

   As such, I ended up removing this feature as the additional work required was too high for this project.

   phrasing?

2. I instead instituted a simpler heuristic using bounded boxes (See Section 2.4.1). Using the `Luxor` library[17], I was able to detect whether two bounded boxes intersected, if they did not, further checks can be skipped.

   Merge these first 2?

3. If two curve segments have already been checked for intersection, why bother checking them again?

   This question was solved by trading computation time for memory, by constructing a hash table linking curve pairs to a tuple of intersection curve segments (if present) and a boolean, when checking two curve sections, if they already exist in the hash table the remaining computation can be skipped with the pre-computed result returned instead.

   In most cases a check is performed at least twice. Given two candidate solutions for two distinct agents B_1 and B_2, when evaluating the fitness of B_1 it is checked for intersections with B_2 and equally when evaluating the fitness of B_2 B_2 is checked against B_1, thus buy storing the first result, the second check can be skipped.

   In reality, many curve segments are found repeatedly inside of populations and as such many more duplicate checks can be skipped through this method.

4. I implemented a recursion depth limit so as to introduce an upper bound in computation before the function returns false. Without this I found that often the checks would repeat until it was searching for intersections between infinitesimally small curve sections.

5. I was also able to reduce the runtime of this function via the use of threading. Upon a subdivision two more threaded tasks are spawned and the lazy disjunction of their results returned. The optimal case for this approach is that the intersection occurs early on in the curve as the task results must be fetched sequentially in the order that they were spawned.

remove this sentence?

My method keeps track of the divisions made and using this keeps track of the t value which maps P_n from the subcurve to the initial curve. The values of t are then returned if a intersection is found, this allows for the distances from the origin points to the point of intersection to be easily calculated using De Casteljau's algorithm along with my function for finding the length of a Bézier curve.

An illustration of the recursive subdivision method described above can be seen in Figure 4.9

4.3 Macro-Level Planning

Title?

The next stage in development is to attempt to implement the wrapper to solve Problem 1 using the solution to Problem 2. I.e. to go from planning for multiple agents in a single section of road to planning for multiple agents across a network of interconnected roads.

4.3.1 Road Graph Construction

As specified in Problem 1, we require a description of the road space as a graph, $\mathcal{R} = (V, E)$ of intersections, V and road segments E

Should I define it as $\mathcal{R} = (I, R)$?

.

This is a malleable definition allowing for a lot of information to encapsulated whilst maintaining an abstract canonical description compatible with a swathe of mathematics through graph theory.

wordy?

I decided to use a mixture libraries to construct my road network: `Graphs.jl`[18], `LightGraphs.jl`[19] and `SimpleWeightedGraphs.jl`[20]. The graph structures found in `Graphs.jl` allow for a lot of data (The entirety of the `Road` structure can be stored as edge metadata) to be encapsulated but do not offer the same functionality as those found in `LightGraphs.jl`, `SimpleWeightedGraphs.jl` utilises the `LightGraphs.jl` format but allows for weighted edges when applying the various standard graph-based algorithms (including Dijkstra), as such I created my own helper functions to convert between the two formats, which is a relatively simple process of filtering data into a new, more restrictive, structure.

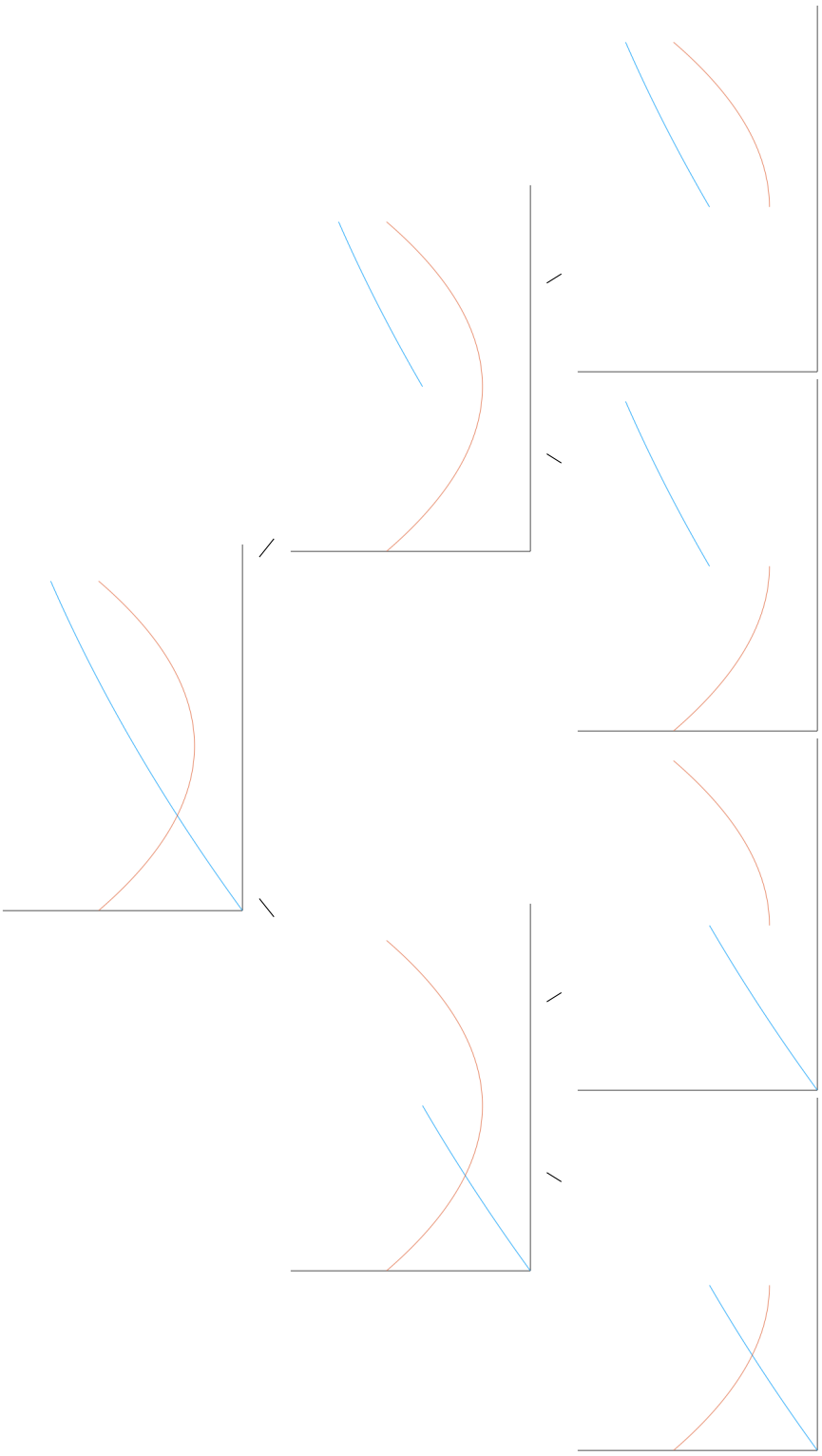


Figure 4.9: Illustration of Bezier Intersection recursive subdivision method (Recursion depth =2)

In the simplified weighted digraph format, the edges are weighted by their length. Going forward it would be possible to incorporate more advanced heuristics into this, mimicking the method by which applications such as Google Maps plan routes. This could include congestion, road surface quality, known planned road obstruction such as maintenance or a predicted large influx of vehicles, for example the exodus of people from a large sports arena.

A visualisation of this format can be seen in Figure 4.10 with edge names and their respective weights labelled.

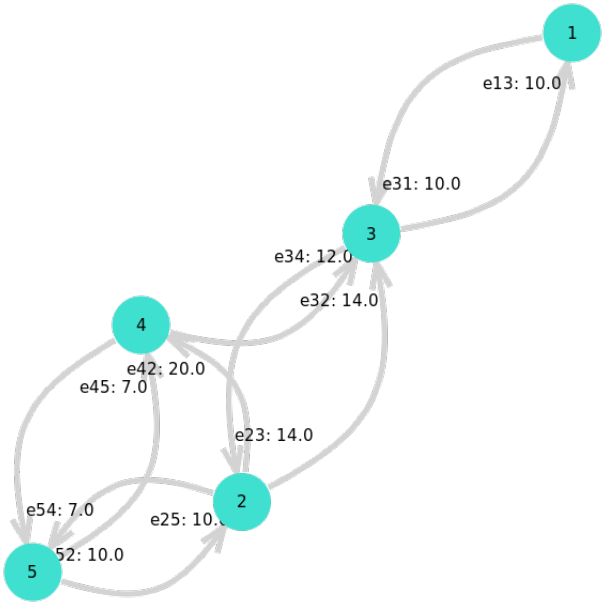


Figure 4.10: Example Road Graph, edge names take the form e<start><end>: <edgeweight>

With the graph constructed the next stage is to plan what I will refer to as the *macro* routes, i.e. the set of edges the agent must travel along $\{e_1, \ldots, e_m\} \subseteq E$ to reach its destination intersection, $d \in V$.

4.3.2 Macro-Route planning

Macro-route planning, as described in Problem 1, is the process of taking a set of intersection pairs corresponding to agents and producing the set of edges which connect the vertex pairs in the shortest distance. This task is almost the exact specification for Dijkstra's algorithm [21] for finding shortest paths in a connected digraph and as such this is the algorithm I employed to solve it.

The `LightGraphs.jl` library already implements this algorithm and the weighted element is incorporated by the `SimpleWeightedGraphs.jl` sub-

library. As previously mentioned, the edges of my road-graph are weighted by their lengths.

For example the following construction of inputs for Problem 1 over the graph seen in Figure 4.10:

$$A = \{a_1, a_2, a_3, a_4\}$$
$$\mathcal{V} = [(1,4),(4,2),(1,4),(3,5)]$$

Would yield the following abstract routes for the agents:

$$\begin{aligned} &P = \{ \\ &a_1 \mapsto \{1,3,2,5,4\}, \\ &a_2 \mapsto \{4,5,2\}, \\ &a_3 \mapsto \{1,3,2,5,4\}, \\ &a_4 \mapsto \{3,2,5\} \\ &\} \end{aligned}$$

The next stage in the process is to group these agents into *planning groups* i.e. groups in which agents will occupy the same road at the same time thus requiring cooperative planning.

4.3.3 Agent Grouping

When planning for multiple agents across multiple road spaces, routes may share the same stretch of road during route execution.

In the above example, it is trivial to see that agents a_1 and a_3 will share the same road at each stage of their route as they are following the same abstract path. We however, must also be able to determine whether agents a_1 and a_4 share road $e25$, it occurs in both of their routes but one agent may have left that stretch of road before the other enters.

This problem is solved using the algorithm seen in Algorithm 2

do I need to make it more obvious that these algorithms are my own work? Are they clear enough?

. For instance, on the example input above, we would expect to see the following grouping:

$$(3,2) \mapsto \{\{a_4, a_1, a_3\}\},$$
$$(4,5) \mapsto \{\{a_2\}\},$$
$$(2,5) \mapsto \{\{a_3, a_1\}, \{a_4\}\},$$
$$(5,2) \mapsto \{\{a_2\}\},$$
$$(1,3) \mapsto \{\{a_3, a_1\}\},$$
$$(5,4) \mapsto \{\{a_3, a_1\}\}$$

Where you can see a_4 occupies edge $e25$ at a time separate from agents a_1 and a_3.

Algorithm 2: Path Grouping, `getPathGroupings`

Input:

- a road network graph $\mathcal{R} = (V, E)$
- a macro-path for each agent, P.

```
Initialise map of roads, roads
for each road, r ∈ E do
    roads[r] = [ ] ;          // Initialise list of agent groups
for each agent's macro-path, i ∈ P do
    Construct a running total of distance for each edge.
    for each edge, e ∈ E in the macro-path do
        ;    // Initialise routes sharing edge e with agent i
        microPlanAgents = [ i ]
        for each other agent's macro-path, o ∈ P\i do
            if e ∈ o then
                ;   // routes i and o share an edge (e) at some
                 point
                if length of i from origin to end of e > length of o
                 from origin to start of e then
                    ; // routes i and o occupy the edge e at the
                     same time
                    append(microPlanAgents, o)
                else
                    ;    // route i exits edge e before o enters
                    continue
        append(roads[e], microPlanAgents)
return roads;       // A map of edges to a list of lists of
 routes sharing that edge at the same time.
```

Once these grouping have been constructed, the next stage is to plan the low-level curves representing the paths each agent must take through each road segment, avoiding any agents it shares a given road segment with.

4.3.4 Multi-agent route planning

title?

This process is a wrapper around the previously implemented parallel planner described in 4.2. It follows the algorithm outlined in Algorithm 3.

Algorithm 3: Macro-route planner

Input:

- set of start-goal pairs for each agent, $\mathcal{V}$
- a graph representing a road network, $\mathcal{R}$

$P = djikstraShortestPath(\mathcal{R}, \mathcal{V})$
pathGroupings = `getPathGroupings`$(\mathcal{R}, P)$
routes = [] ; `// initialise routes array as list of paths through each road segment specified by macro-route in` P
for *each macro-path,* $p \in P$ **do**
  for *each edge* $e \in p$ **do**
    concurrentAgentSets = pathGroupings[e]
    for *concurrentAgents* $\in$ *concurrentAgentSets* **do**
      construct start and goal positions for each agent. This process requires further thought/ research **better way to talk about this?**
      paths = parallelPlanner(startPositions, goalPositions, e) ;
      `// Parallel planner, solution to Problem 2`
      for *each agent* $a_i \in \mathcal{V}$ **do**
        append(routes[i], paths[i])
return *routes*

phrasing about s/e position calculation on alg 3

My approach vastly simplifies the problem of intersection navigation and linking the routes between road segments, essentially assuming all road segments are sections of a single long road which line up exactly. Papers such as "Automated Optimization of Intersections Using a Genetic Algorithm" by Cruz-Piris et al.[10] begin to tackle this problem through the use of cellular automata (building on the work of Maerivoet and De Moor[22]

necessary?

) and GAs (See Section 3.1.1) but substantial work would be required to link our two systems together.

4.4 Language Choice

decide whether to remove this, I am thinking yes but last para is interesting, maybe move to evaluation

I have chosen to implement my approach using the Julia language project[23].

Julia is a relatively new language first developed in 2012 by Jeff Bezanson, Stefan Karpinski and Viral Shah. It is a multi-paradigm language allowing for functional, object oriented (OO) and meta programming approaches to problems. I will mainly be using it for it's functional and OO capabilities.

Julia operates using multiple dispatch similar to languages such as Haskell. It interoperates with C and Fortran codebases without the need of middleman bloat. This fact allows it to utilise the extensive high performance C libraries for floating point operations. Julia is eagerly evaluated, uses a Just in time compiler and has a garbage collector.

Julia features a syntax similar to both Python and Matlab with performance on par with C. As I am already very familiar with python and have studied functional programming in a number of modules; I found this language very quick and intuitive to learn and the resulting code to be clean, idiomatic and fast.

A real-world deployment of a system based on my research would undoubtedly be required to run on small, relatively low performance, embedded systems and as such Julia may not be appropriate here. A language such as C or Rust may be used instead.

Julia also has distributed computation facilities. This sort of functionality could be extremely useful in a system such as mine as it could allow for computation to be spread across the agents themselves, removing the need for a central planning centre which could be a single point of failure.

5 Results

ID	Description	Link
1	Single Agent Results, coloured by opposite surface	url
2	Multi agent results	url
3	Multi agent results, coloured by opposite surface	url
4	Multi agent results, coloured by opposite surface, fitness threshold = 40	url
5	Multi agent results, with fitness-planning time overlayed, fitness threshold=100	url

Figure 5.1: External links to dynamic plots

Is this a clear way of formatting? I would reference the ID when talking about a plot. I would still include an image as a figure

Due to the high dimensionality of my search space, I cannot visualise the objective function of my GA.

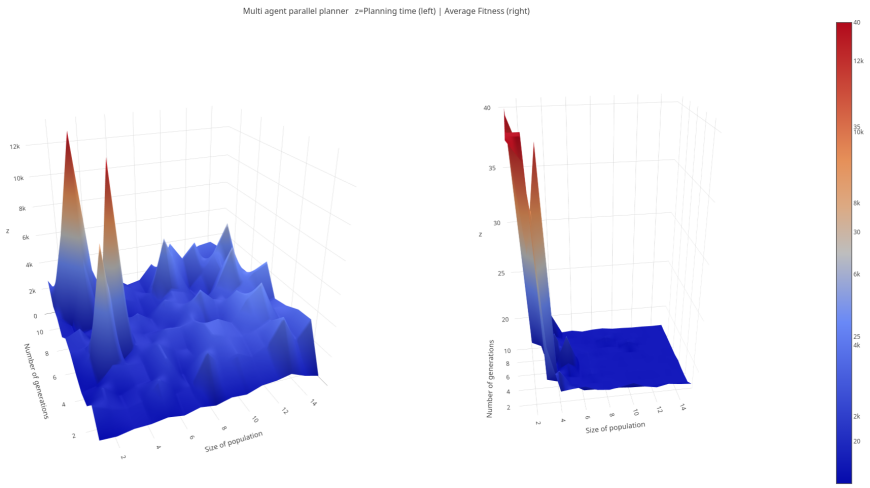


Figure 5.2: Multi agent planning number of generations against size of population against planning time (left), fitness limited at 40 (right)

Check units for planning time + add link to hosted dynamic version

Check units for planning time + add link to hosted dynamic

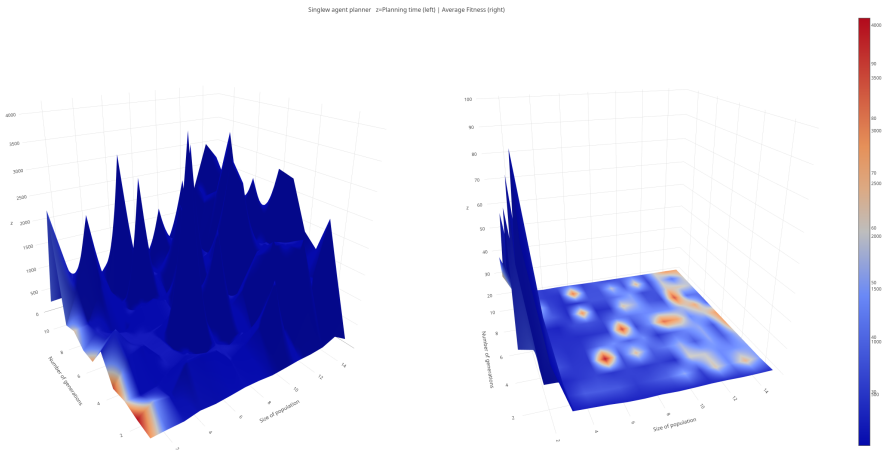


Figure 5.3: Single agent planning: number of generations against size of population against planning time (left), fitness (right)

6 Evaluation

6.1 Genetic Algorithms

The core of my approach to solving the problems outlined in Chapter 1 was creating a Genetic algorithm to evolve populations of candidate routes, returning the fittest once the termination criteria are met.

GAs are transparent, probabilistic approaches to optimisation problems. As such, it is much easier to reason about and predict their output when compared with more traditional *black box* approaches such as neural networks.

Whilst a poor choice of training data can lead to unintended/ unpredictable behaviour from approaches like neural networks, they have the advantage that most of their compute time is used when constructing the initial model, subsequent usage of these models requires little compute time. Whereas, GAs must run the entirety of the *learning* process from scratch whenever a new route or set of routes is required. In an application where the system sees a high number of unique requests, this compute time can quickly amount to much longer than the training time for a neural network.

6.1.1 Genetic Operator Performance

During development I implemented two different operators in each category, but there are many other approaches proposed in academic literature. Given more time, I would have liked to implement more and present a more empirical evaluation of each.

Selection

In a single generation, over three populations of 15 individuals, my ranked selection operator ran 3 times totalling $97.4\mu s$ or an average of $32.5\mu s$ per run.

As you can see in Figure 4.5, my ranked selection operator performs its task well, removing the obviously less fit individuals in favour of more copies of fitter ones. This can be seen by the removal of the line that dips below the x axis (in this example the bottom road boundary was defined as $b_1(x) = 0$) and the fact that duplicate routes are found as indicated by the 3rd graph of unique routes showing fewer individuals than the second.

Ranked selection compared with fitness proportional (roulette wheel selection) is much more predictable, it may not explore as much of the search space but it is more likely to thoroughly explore a single area. Most other

selection operators seem to focus on maintaining a diverse population so as to not get stuck in local minima.

Mutation

The mutation operators I implemented were Uniform and Gaussian.

I found Gaussian to perform better in cases where a route may be close to optimal in the phenotypic space, i.e. with minimal changes to trajectory, it would be optimal. In such cases the genotypic fitness may not accurately represent this, a route that collides with another or passes through infeasible space will suffer from a large genotypic fitness penalty possibly encouraging it to be removed from the *gene pool*. Gaussian mutation, preferring mutated points closer to their initial position can be effective as moving such routes closer to the optima.

However, in cases where the initial population generation has created all routes far from the optimal, Gaussian mutation can struggle to generate mutated points extreme enough to direct the GA towards the minima.

Part of the problem with Gaussian mutation, and mutation in general on n-degree Bezier curves, is that even a relatively major control point movement may cause only minor changes to the overall trajectory of the curve in cases where n is high.

An example of a relatively large control point mutation leading to a minor direction change can be seen in Figure 4.6.

It is possible that an approach incorporating a form of Simulated Annealing could help to broadly explore the search space in early generations before refining solutions in a found minima in latter generations. This could operate by applying a different mutation operator such as Uniform mutation in the first 60% of generations before swapping to Gaussian when we would expect our algorithms to have found some local minima.

In a single generation, over the same 3 sets of 15 individuals, my Gaussian mutation operator ran 3 times totalling $1.8ms$ runtime, an average of $601\mu s$. This is an insignificant amount of time when compared to the overall runtime of this task which stands at 34.3.

Crossover

I only implemented a single form of crossover: simple (one point) crossover.

Implement another crossover operator to talk about ?

Fitness

As previously mentioned the most important operator, and the one I spend the most time working on, is the fitness function.

This acts as the objective function for the algorithm as it seeks to minimise its value across multiple agents over multiple generations.

This operation, especially when modified to detect collisions, was the source of most of the runtime of my project. In the toy example of 3 sets of 15 agents across a single generation, the fitness function accounted for a large proportion of the runtime at 23.1 across 3 calls, an average of 7.69 seconds per invocation. This is after all my attempts to speedup the process (See Section 4.2.1).

The final incarnation of my fitness function can be thought of as two separate parts:

1. The *base fitness* i.e. the fitness when considered in isolation in the road space.

   This calculation again can be thought of as being comprised of 3 parts as outlined in Equation 4.1:

   In total this portion of the function ran in an average of $105ms$ or 0.00092% of the fitness function runtime

   (a) Route length

   This procedure had an average runtime of around $6.24\mu s$ or $5.47 \times 10^{-8}\%$ of the fitness function runtime

   (b) infeasible distance length taking an average of $59.5ms$ to run

   (c) Close proximity distance length

2. The collision penalty

   Collision detection as previously stated was a major source for complexity in my project. However, after a lot of tweaking and time saving measures, in this toy example the runtime for the collision detection stands at an average of $34.9ms$, less than the average runtime of the infeasible distance calculation.

Is this all too boring?

6.2 Bézier Curves

expand on this section, talk about issues of finding intersection, possible GPU applications

Bézier curves have been utilised in this project to encode and represent the route of a vehicle. As mentioned in Section 2.2, there are many reasons I originally selected them for this task. However, over the course of implementation and testing, a number of downsides have been presented.

1. Objective numerical approaches with Bézier curves are often complicated, expensive and do not generalise well to n control points.

correct word?

This leads to many heuristics, and approximations being employed to save computation. Approximations and assumptions in a system as the one proposed in this report, are sub-optimal and could potentially lead of undesired behaviour which could ultimately have dire consequences if such a system were to be deployed.

Other research such as that by Cai & Peng[2] takes a different approach, using discrete, grid-based search spaces in which routes are made up of a series of connected straight line segments. This approach removes much of the complexity from my solution but introduces its own concerns.

The routes generated by Cai & Peng's approach are intended to be executed by autonomous robots, so no thought has been given to potential passengers. Consequently, these routes would require smoothing as a post-planning process, re-introducing complexity.

Another possible representation is the approach taken by Cruz-Piris et al.[10] which involved representing the section of road, in their case an intersection, as a cellular automata in which a single vehicle can occupy a single cell at any given point in time.

does this need to be an enumerated list?

There were however, also some advantages and nice properties of Bézier curves which lent themselves to the task.

Their relatively simple abstract construction as a series of control points proved easy to concretely represent as a genotype. This made the creation of the various genetic operators relatively simple, requiring little pre or post-processing.

They are also capable of representing a high complexity of curve in a relatively simple and concise manner. This makes code much more approachable and algorithms easier to digest.

6.2.1 Cooperative Planning

My solution to the problem of planning n non-colliding routes for n agents was so wrap my existing `GA` function in a cooperative *layer*. This cooperative layer relied on a function for detecting collisions which had extremely high overhead, at one point causing around 50x slowdown in the running time of the function. Detecting intersections between two Bézier curves is a non-trivial task with the best methods taking the same approach of recursive subdivision that I utilised.

make mention of possible GPU implementations such at in [3], modern enterprise GPUs have around 4000-10000 cores, approximately the max number of curve splits and comparisons in a binary check of depth 6. Being able to do this in a single cycle would result in a huge speedup, paper uses Titan X

7 Conclusion

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Appendices